

Finding ORFs

Task Name: find-orfs

Searches for Open Reading Frames (ORFs) in nucleotide sequences and saves the regions found as annotations.

Parameters:

in — semicolon-separated list of input files. [String, Required]

out — output file with the annotations. [String, Required]

name — name of the annotated regions. [String, Optional, Default: "ORF"]

min-length — ignores ORFs shorter than the specified length. [String, Optional, Default: 100]

require-stop-codon — ignores boundary ORFs that last beyond the search region (i.e. have no stop codon within the range). [Boolean, Optional, Default: false]

require-init-codon — allows ORFs starting with any codon other than terminator. [Boolean, Optional, Default: true]

allow-alternative-codons — allows ORFs starting with alternative initiation codons, accordingly to the current translation table. [Boolean, Optional, Default: false]

Example:

```
ugene find-orfs --in=human_T1.fa --out=result.gb --require-init-codon=false
```